

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 18:07:30 ; Search time 13.42 Seconds
(without alignments)
1009.824 Million cell updates/sec

Title: US-69-686-020A-2
Perfect score: 1819
Sequence: 1 MALEONQSTDYTYEENEMNG.....VEEPPDSEGPTEPTSTPSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 10524 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	1819	100.0	350	1	CKRB_HUMAN
2	1620	89.1	350	1	CKRB_BOVIN
3	659	36.2	378	1	CKR7_HUMAN
4	650	35.7	378	1	CKR7_MOUSE
5	639	35.1	359	1	CKR9_MOUSE
6	637	35.0	357	1	CKR9_HUMAN
7	605	33.3	367	1	CKR6_MOUSE
8	583	32.1	374	1	CKR6_HUMAN
9	581	31.9	342	1	CKR6_CERAE
10	571	31.4	343	1	CKR6_MACNE
11	569	30.8	342	1	CKR6_MACNE
12	560	30.8	342	1	CKR6_HUMAN
13	537.5	29.5	360	1	CKR4_HUMAN
14	534.5	29.4	360	1	IL8B_HUMAN
15	529.5	29.1	353	1	IL8B_HUMAN
16	525	28.9	362	1	IL8B_PANTR
17	524	28.8	354	1	CKR4_HUMAN
18	523	28.8	354	1	CKR4_HUMAN
19	522.5	28.7	353	1	IL8B_GORGO
20	522.5	28.7	353	1	CKR4_HUMAN
21	522.5	28.7	360	1	CKR4_MOUSE
22	521.5	28.6	353	1	IL8B_MOUSE
23	520.5	28.6	356	1	IL8B_CANFA
24	512	28.1	354	1	CKR4_MOUSE
25	511	28.1	354	1	IL8B_RABIT
26	511	28.1	354	1	IL8B_RABIT
27	504	27.7	360	1	CKR2_MOUSE
28	501.5	27.6	355	1	IL8B_RABIT
29	501.5	27.6	358	1	CKR3_CAVPO
30	500.5	27.5	352	1	CKR4_HUMAN
31	499.5	27.5	353	1	CKR4_BOVIN
32	499.5	27.5	360	1	IL8B_BOVIN
33	498.5	27.4	352	1	CKR4_PAPAN

34	498.5	27.4	352	1	CKR5_CERNO	062743 cercocebus
35	498.5	27.4	353	1	CKR4_FELCA	P56498 felis silve
36	497.5	27.4	350	1	IL8A_GORGO	P55919 gorilla gor
37	495.5	27.2	352	1	CKR5_CERAE	P56493 cercopithec
38	494.5	27.2	352	1	CKR4_CERNO	062747 cercocebus
39	493.5	27.1	352	1	CKR4_MACFA	028474 macaca fasc
40	493.5	27.1	352	1	CKR4_MACMU	P79394 macaca mula
41	492.5	27.1	359	1	CKR3_RAT	P54814 rattus norv
42	492.5	27.1	359	1	IL8B_RAT	P35407 rattus norv
43	491.5	27.0	352	1	CKR5_PAPHA	P56441 papio hanad
44	491.5	27.0	352	1	CKR5_PYGRI	097880 pygathrix b
45	490.5	27.0	352	1	CKR5_MACMU	P79436 macaca mula

ALIGNMENTS

RESULT ID	CKRB_HUMAN	STANDARD:	PRT:	350 AA.
AC	09NPB9:			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	C-C chemokine receptor type 11 (C-C CRK-11) (CCR-11)			
DE	(Chemokine receptor-like 1) (CCR1L) (CCX CRK).			
GN	CCR1L OR CCRP2 OR VSHK1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20200450; PubMed=10734104;			
RA	Schweickart V.L., Epp A., Raport C.J., Gray P.W.;			
RT	"CCR1L is a functional receptor for the monocyte chemoattractant			
RT	protein family of chemokines.";			
RL	J. Biol. Chem. 275:9550-9556(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=2017178; PubMed=10706668;			
RA	Gosling J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z.,			
RA	Schall T.J.;			
RT	"Cutting edge: Identification of a novel chemokine receptor that binds			
RT	dendritic cell- and T cell-active chemokines including ELC, SLC, and			
RT	TECK.";			
RL	J. Immunol. 164:2851-2856(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20231748; PubMed=10767544;			
RA	Khoja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamala V.;			
RT	"Cloning of CCR1L, an orphan seven transmembrane receptor related to			
RT	chemokine receptors, expressed abundantly in heart.";			
RL	Gene 246:229-238(2000).			
CC	- FUNCTION: RECEPTOR FOR SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4.			
CC	SCYA19/MIP3B/ELC, SCYA21/SLC AND SCYA25/TECK.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN HEART. LOWER			
CC	EXPRESSION IN LUNG, PANCREAS, SPLEEN, SMALL INTESTINE AND FETAL			
CC	TISSUES.			
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL, AF193507; AAF61299.1; -			
DR	EMBL, AF233281; AAF44751.1; -			
DR	EMBL, AF110640; AAF59827.1; -			

InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPS.
 DR PROSITE: PS00237; G-PROTEIN_REC_P1.1;
 DR PROSITE: PS0262; G-PROTEIN_REC_P2.1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 43 63 POTENTIAL.
 FT DOMAIN 64 87 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 88 108 POTENTIAL.
 FT DOMAIN 109, 113 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 114 134 POTENTIAL.
 FT DOMAIN 135 154 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 155 175 POTENTIAL.
 FT DOMAIN 176 201 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 202 222 POTENTIAL.
 FT DOMAIN 223 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 241 261 POTENTIAL.
 FT DOMAIN 262 289 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 290 310 POTENTIAL.
 FT DOMAIN 311 350 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID-112 184 BY SIMILARITY.
 SQ SEQUENCE 350 AA; 39913 MW; 8E26049D2D5757C8 CRC64;

Query Match 100.0%; Score 1819; DB 1; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.3e-104;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR 1 MALEONOSTDYEEENENGTVDYDQVELICIKEDVREFAKFLPVLFTIVFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENENGTVDYDQVELICIKEDVREFAKFLPVLFTIVFVIGLAGNS 60
 QY 1 MVAIAYAYKKORTKTDVYILMLAVADLLFTLPFWANAVHGVNGLKIMCKITSAIYT 120
 DB 61 MVAIAYAYKKORTKTDVYILMLAVADLLFTLPFWANAVHGVNGLKIMCKITSAIYT 120
 QY 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGVGPCKMIIICFCVMAAILISPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGVGPCKMIIICFCVMAAILISPOLVFTVND 180
 QY 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGVGPCKMIIICFCVMAAILISPOLVFTVND 180
 DB 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGVGPCKMIIICFCVMAAILISPOLVFTVND 180
 QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKNPKNISRLK 240
 DB 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKNPKNISRLK 240
 QY 241 VLLFVYVIFYTQLPYNIIVKFCRAIDIIYSITSCNMSKRDIAIQYTESIALFHSCLNP 300
 DB 241 VLLFVYVIFYTQLPYNIIVKFCRAIDIIYSITSCNMSKRDIAIQYTESIALFHSCLNP 300
 QY 301 ILYVFMGASFKNYVAKKATGSMRQROSVPEPDESGTEPTSTFSI 350
 DB 301 ILYVFMGASFKNYVAKKATGSMRQROSVPEPDESGTEPTSTFSI 350

RESULT 2
 CRRB_BOVIN STANDARD; PRT; 350 AA.
 AC P35350;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE C-C chemokine receptor type 11 (C-CR-11) (CC-CR-11) (CCR-11)
 DE (Possible gustatory receptor type B) (ppri protein).
 GN CCR11.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE= Tongue.
 RX MEDLINE=93326166; PubMed=8392843;
 RA Matsuo K., Mori T., Sato T., Kurihara K.;
 RT Identification of novel members of G-protein coupled receptor
 RT Superfamily expressed in bovine taste tissue.";
 RL Biochem. Biophys. Res. Commun. 194:504-511(1993).
 CC -1- FUNCTION: RECEPTOR FOR SCYB2/MCP1, SCYB8/MCP2, SCYB13/MCP4,
 CC SCYB19/MIP3B/ELC, SCYB21/SIC and SCYB25/TECK (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN CIRCUMVALLATE AND FUNGIFORM
 CC PAPILLAE, OLFACTORY EPITHELIUM AND LUNG. LOWER EXPRESSION IN
 CC LIVER, KIDNEY AND TONGUE EPITHELIUM BEARING NO TASTE PAPILLAE.
 CC VERY LOW EXPRESSION IN THE CEREBRAL CORTEX OF THE BRAIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: S63848; AAB27547.1; -
 DR PIR: JN0621; JN0621.
 DR GCRDB: GCR_0757; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPS.
 DR PROSITE: PS00237; G-PROTEIN_REC_P1.1;
 DR PROSITE: PS0262; G-PROTEIN_REC_P2.1;
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation.
 FT DOMAIN 1 41 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 42 66 1 (POTENTIAL).
 FT DOMAIN 67 79 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 80 99 2 (POTENTIAL).
 FT DOMAIN 100 113 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 114 135 3 (POTENTIAL).
 FT DOMAIN 136 153 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 154 175 4 (POTENTIAL).
 FT DOMAIN 176 199 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 200 222 5 (POTENTIAL).
 FT DOMAIN 223 241 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 242 265 6 (POTENTIAL).
 FT DOMAIN 266 283 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 284 306 7 (POTENTIAL).
 FT DOMAIN 307 350 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 112 184 BY SIMILARITY.
 SQ SEQUENCE 350 AA; 40008 MW; E46BF942F3919C82 CRC64;

Query Match 89.1%; Score 1620; DB 1; Length 350;
 Best Local Similarity 86.0%; Pred. No. 1.8e-92;
 Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENENGTVDYDQVELICIKEDVREFAKFLPVLFTIVFVIGLAGNS 60
 DB 1 MAVEYNSOTDYEEENENGTVDYDQVELICIKEDVREFAKFLPVLFTIVFVIGLAGNS 60
 QY 61 MVAIAYAYKKORTKTDVYILMLAVADLLFTLPFWANAVHGVNGLKIMCKITSAIYT 120
 DB 61 TVAIAYAYKKORTKTDVYILMLAVADLLFTLPFWANAVHGVNGLKIMCKITSAIYT 120
 QY 121 LNFVSGMOFLACISIDRYVAATKVPSSGSGVGPCKMIIICFCVMAAILISPOLVFTVND 180
 DB 121 VNFVSGMOFLACISIDRYVAATKVPSSGSGVGPCKMIIICFCVMAAILISPOLVFTVND 180
 QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKNPKNISRLK 240
 DB 181 KARCVPIPFYHGTSMKASIQMLEICIGFVVPFLMGVCYFTARTLMKNPKNISRLK 240

Query Match	Best Local Similarity	Score	DB 1;	Length
Matches 144; Conservative	38.7%;	659;	DB 1;	378;
		Pred. No. 7.4e-34;		
	66; Mismatches 124; Indels 38; Gaps			
Query	1	MALENOSTDYEEENENGTVDYSQVELCEKEDREFAKVFLPELITVIVIGLAGNS	60	
Db	21	VELCODEVTDDIDIGNT---TVDYLFESLCKKDYRNFANFLPMSTICFVGILGNG	77	
QY	61	MVAVIAYAYKKORTVDYIILNLAVALDLLETPLEFMAVNAVHGVGLKIMKITSALYT	120	
QY	78	LVLLVLYIYFKRKLTMTDLYILNLAVADLLELLETFPMVSAKSNVFGVHPCKLPAIYK	137	
Db	121	LVFVSGMOFLACISIDRYAVATKVS-----QSGVCKPCMIICFCVMAAILISDOLVY	176	
QY	138	MSFSGMLLTICISMRVAVIQAANSAHRHRAVLLISKLSGVGIMVILATVLSIPELAYS	197	
QY	177	TVNDA-----RCIPIFPRYLGTSMKALIMLEICIGFVPLNGVCYTARPMKMP	231	
Db	198	DLGRSSSQAMCSLITEH---VEAFITLQVAAQMTIGFLPLAASFCLYVITRLLAR	254	
QY	232	NKISRPLKVLTVVIVITVQLPYNIKFCRAIDIIISLTSCMSKRMIDAIDVETESI	291	
Db	255	NFERKAKIVIIAAVVVIVITVQLPYNGVLAQTVANFNITSSTCLSLQMLNADVYISL	314	
QY	292	ALFHSCAMPILLYVEGASFKNYVMVAKYK-----SW-----RRGRSVEEPPD	337	
Db	315	ACVRCVAFPLTAFIAGVFKRNDLEKFLKDGLCLSOEQLRQMSCRHIRSSMSYE-----	369	
QY	338	SEGPTEPTSTPS	349	
Db	370	---AETTTTS	377	
RESULT	4			
CKR7_MOUSE	ID	CKR7_MOUSE	STANDARD;	PRT; 378 AA.
AC	P4774;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	C-C chemokine receptor type 7 precursor (C-C CR-7) (CC-CR-7) (CCR-7)			
DE	(MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1)			
DE	(EBI1).			
GN	CCR7 OR CCR7 OR EBI1 OR EBI1.			
OS	Mus musculus (Mouse).			

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OM protein - protein search, using sw model

Run on: August 6, 2002, 17:57:40 ; Search time 32.78 Seconds
(without alignments)
1185.962 Million cell updates/sec

Title: US-09-686-020a-2

Perfect score: 1819
Sequence: 1 MALBQNSQSDYYEENEMNG.....VEPPFDESGTEPTSTPSI 350

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq.032802.*
2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.*
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21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.*
23: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1819	100.0	350	AAV57290	Human BGCKr protei
2	1819	100.0	350	AAV17435	Human signal pepti
3	1819	100.0	350	AAW93169	Human HPIA041 prot
4	1819	100.0	350	AAV94325	Human seven transm
5	1819	100.0	350	AAAG80119	Human CCR11 protei
6	1819	100.0	350	AAU08994	Human G protein-co
7	1819	100.0	350	AAAG7237	Amino acid sequenc
8	1819	100.0	382	AAAG52389	Human chemokine re
9	1814	99.7	349	AAW93170	Human HPIA041 prot
10	1814	99.7	350	AAV30125	A human seven-pass
11	1810	99.5	350	AAV71301	Human orphan G pro

12	1810	99.5	350	21	AAAB02835	Human G protein co
13	1808	99.4	350	21	AAAB37788	Human TSC7. Homo
14	1728	95.0	333	20	AAV57289	Human BGCKr protei
15	1620	89.1	350	22	AAAG57238	Amino acid sequenc
16	1591	87.5	350	20	AAV57291	Mouse BGCKr protei
17	1275	70.1	246	20	AAV57292	Human BGCKr protei
18	1257	69.1	242	22	AAW99949	Human expressed po
19	1212	66.6	263	20	AAV30126	A seven-pass trans
20	862	47.4	164	22	ABB11162	Human orphan GPCR
21	862	47.4	164	22	AAW79310	Human protein, SEO
22	824	45.3	159	21	AAAB41786	Human ORFX ORF1550
23	761	41.8	175	22	AAW99976	Human expressed po
24	761	41.8	175	22	ABBI0276	Human cDNA seq ID
25	761	41.8	175	22	AAU18115	Novel human uterin
26	761	41.8	175	22	AAU18361	Human endocrine po
27	761	41.8	175	22	AAU18669	Renal and cardiova
28	761	41.8	175	22	AAU21655	Novel human neopla
29	659	36.2	358	15	AAAB3745	Partial sequence o
30	659	36.2	358	21	AAAB21689	Human 7TM receptor
31	659	36.2	378	19	AAW48724	Human V21 seven tr
32	659	36.2	378	22	AAAB21688	Human 7TM receptor
33	659	36.2	378	22	AAAB80114	Human CCR7. Homo
34	659	36.2	378	22	AAAB50859	Human CCR7. Homo
35	659	36.2	410	15	AAAB53743	Putative seven tira
36	659	36.2	410	19	AAW48723	Polypeptide sequen
37	659	36.2	410	21	AAAB21687	Genomic clone of 7
38	659	36.2	569	22	ABG12373	Novel human diagno
39	656	36.1	378	15	AAAB5744	Putative seven tira
40	655	36.0	378	21	AAV90663	Human mutant G pro
41	653	35.9	378	21	AAV90629	Human G protein-co
42	650	35.7	378	22	AAAB21699	Human 7TM receptor
43	643	35.3	369	22	AAAG80116	Human CCR9a protei
44	643	35.3	378	15	AAAB54079	Epstein Barr virus
45	643	35.3	378	19	AAW56164	G-protein coupled

ALIGNMENTS

RESULT 1
AAV57290 standard; Protein; 350 AA.
XX AAV57290;
AC AAV57290;
XX 05-JUN-2000 (first entry)
XX Human BGCKr protein.
DE Human BGCKr protein.
XX BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;
XX cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
XX anti-allergic; antiviral.
XX Homo sapiens.
OS Homo sapiens.
XX W09952945-A2.
PN W09952945-A2.
XX 21-OCT-1999.
XX 16-APR-1999; 99WO-US08395.
XX 16-APR-1998; 98US-0061753.
XX 16-APR-1999; 99US-0061753.
XX (MILL-) MILLENIUM PHARM INC.
XX Gonzalo JA, Gutierrez-Ramos JC;
XX WPI: 1999-620375/53.
XX N-PSDB; AA290528.
XX New nucleic acid encoding human BGCKr receptor, used e.g. for
XX modulating inflammation and tumor growth

XX Claim 8; Fig 2A-B; 123pp; English.

PS The invention relates to a human BGCR protein, a G-protein coupled
 CC receptor. The BGCR protein can be expressed by standard recombinant
 CC methodology. BGCR are receptor proteins possibly involved in modulation
 CC of proinflammatory or stimulatory functions of chemokines; cell
 CC proliferation, migration, adhesion and targeting, and exocytosis. The
 CC BGCR nucleic acids and derived proteins (or their variants), antibodies
 CC and modulators are potentially useful for modulating inflammation;
 CC chemottractant activity of leucocytes; angiogenesis; cell proliferation;
 CC tumour growth; allergic reactions and entry of human immune deficiency
 CC virus into cells, for therapeutic or prophylactic purposes. They are also
 CC used for diagnosis and in drug-screening assays. The present sequence
 CC represents the full-length human BGCR protein.

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 20; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.6e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYTYEENENMGTYDYSOYELICIKEDVREFAKVELPVLITVIVIGLAGNS 60
 DB 1 maleqngstdyyeenemngtydygyelickedvrefakvllpvlitvfviglaags 60
 QY 61 MVAATAYAYKKQRTKTDVYIINLAVADLLLTLPFMAVNAVHGVNLGKIMCKITSALYT 120
 DB 61 mvaaayaykkqrktldvylinlavadlllftlpfwaavnavhgvnlgkimckitsalyt 120
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGSGVKPCWIIICFCVMAAIIISIPOLVITYVND 180
 DB 121 lnfvsqmgflacisidryavatkvpssgsgvkcwiiicfcvmaaiiisipqlvityvnd 180
 QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVYFLLMGVCYFTARTLTKMPNIRKISRLK 240
 DB 181 narcpiprlylgtsmkallqmlaicigfvyvflimgvcyftartlkmknirksrplk 240
 QY 241 VLLTVVIVYIVQLPYNIYKFCRAIDIIYSLTSCNMSKRDIAIQVETSIALFHSCINP 300
 DB 241 vlltvvivyivqlpyniykfcraidiiysltscnmskrdiaiqvetisialfhscinp 300
 QY 301 ILYVFMGASFKNYVMKAKKYSRROSYEPEPDESGPTSTPSI 350
 DB 301 illyvmgaskfnyvmkakkysrrqsyveepfdepgptstpsl 350

RESULT 2

AAV17435
 ID AAV17435 standard; Protein: 350 AA.

AC AAV17435;

DT 29-JUL-1999 (first entry)

DE Human signal peptide-containing protein SP-16.

KW Human; signal peptide-containing protein; SP; cell proliferation;
 KW cancer; neuronal disorder; immune response; detection.

OS Homo sapiens.

PN W09924463-A2.

PD 20-MAY-1999.

PF 04-NOV-1998; 98WO-US23578.

PR 07-NOV-1997; 97US-0966316.

PA (INCY-) INCYTE PHARM INC.

XX

PI Au-Young J, Lal P, Mathur P, Murry LE, Reddy R;
 XX WPI: 1999-337694/28.
 DR N-PSDB; AAX61288.
 PT CDNA clones encoding signal peptide-containing proteins
 PS Claim 1; Fig 1; 83pp; English.

XX The present sequence represents a human signal peptide-containing
 CC protein (SP), designated SP-16. SP proteins can be used to stimulate
 CC cell proliferation or to treat or prevent cancer. SP antagonists are
 CC also used to treat or prevent cancer, and also for treating or
 CC preventing neuronal disorders or immune responses. Polynucleotide
 CC sequences complementary to the SP-encoding polynucleotides are useful
 CC for the detection of SP-encoding nucleic acid molecules in biological
 CC samples.

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 20; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.6e-195;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEQNSTDYTYEENENMGTYDYSOYELICIKEDVREFAKVELPVLITVIVIGLAGNS 60
 DB 1 maleqngstdyyeenemngtydygyelickedvrefakvllpvlitvfviglaags 60
 QY 61 MVAATAYAYKKQRTKTDVYIINLAVADLLLTLPFMAVNAVHGVNLGKIMCKITSALYT 120
 DB 61 mvaaayaykkqrktldvylinlavadlllftlpfwaavnavhgvnlgkimckitsalyt 120
 QY 121 LNFVSGMOFLACISIDRYAVATKVPSSGSGVKPCWIIICFCVMAAIIISIPOLVITYVND 180
 DB 121 lnfvsqmgflacisidryavatkvpssgsgvkcwiiicfcvmaaiiisipqlvityvnd 180
 QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVYFLLMGVCYFTARTLTKMPNIRKISRLK 240
 DB 181 narcpiprlylgtsmkallqmlaicigfvyvflimgvcyftartlkmknirksrplk 240
 QY 241 VLLTVVIVYIVQLPYNIYKFCRAIDIIYSLTSCNMSKRDIAIQVETSIALFHSCINP 300
 DB 241 vlltvvivyivqlpyniykfcraidiiysltscnmskrdiaiqvetisialfhscinp 300
 QY 301 ILYVFMGASFKNYVMKAKKYSRROSYEPEPDESGPTSTPSI 350
 DB 301 illyvmgaskfnyvmkakkysrrqsyveepfdepgptstpsl 350

RESULT 3

AAW93169
 ID AAW93169 standard; Protein: 350 AA.

AC AAW93169;

DT 24-MAY-1999 (first entry)

DE Human HFINO41 protein.

KW HFINO41; G-coupled receptor; disease susceptibility; diagnosis; immunise;
 KW treatment; FIAO41 protein; gene therapy; immune response; vaccine; HIV-2;
 KW inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;
 KW diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;
 KW hypotension; hypertension; urinary retention; osteoporosis; allergy;
 KW angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;
 KW benign prostatic hypertrophy; psychotic disorder; neurological disorder;
 KW anxiety; manic depression; delirium; dementia; severe mental retardation;
 KW dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;
 KW linkage analysis; gene mapping; human.

OS Homo sapiens.

XX

Wed

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PN EF899332-A2.
PD 03-MAR-1999.
XX
XX 17-FEB-1998: 98BP-0301170.
XX
XX 27-OCT-1997: 97US-0962922.
PR 15-AUG-1997: 97US-0055895.
XX
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX
XX ELLIS CE;
XX
XX WPI: 1999-144803/13.
DR N-PSDB: AAX22557.
XX
XX New G-coupled receptor (HTR041) polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of
PT cancer, HIV infections and Parkinson's disease
XX
XX PS Claim 1: Page 22-23; 27pp; English.
XX
CC This sequence represents a G-coupled receptor, HTR041 which is useful
CC for diagnosing susceptibility to diseases by detecting mutations in the
CC HTR041 gene, and can diagnose diseases associated with HTR041 protein
CC imbalance by determining HTR041 polypeptide expression levels. Agonists
CC and antagonists of the protein can be used in treatment to activate
CC (agonist) or inhibit (antagonist) HTR041 activity, in addition to direct
CC administration of antisense sequences to prevent expression, or HTR041
CC polynucleotides to treat conditions associated with a lack of HTR041
CC protein. Gene therapy may also be used to affect endogenous HTR041
CC polypeptide expression. HTR041 antibodies are useful for inducing an
CC immune response to immunise and prevent disease, and for isolating
CC HTR041 clones or purifying the polypeptides by affinity chromatography.
CC HTR041 polypeptides can be administered directly or as a vaccine to
CC inoculate against disease. Diseases diagnosed, prevented and treated
CC include bacterial, fungal, protozoan and viral infections, particularly
CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; hypertension; urinary
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC asthma; allergies; benign prostatic hypertrophy; and psychotic and
CC neurological disorders, including anxiety, schizophrenia, manic
CC depression, delirium, dementia, severe mental retardation and dyskinesias
CC such as Huntington's disease or Gilles de la Tourette's syndrome. The
CC HTR041 polypeptide is also useful for mapping the gene to a chromosome,
CC allowing gene inheritance to be studied through linkage analysis.
XX
XX Sequence 350 AA:
SQ

```

```

QY 301 ILVFMGASFKNYVMYAKKYGSMRROSGVEEFPDSEPTPTSTFST 350
DB 301 ILYFMGASFKNYVMYAKKYGSMRROSGVEEFPDSEPTPTSTFST 350

RESULT 4
AA94325
AA94325 standard; Protein: 350 AA.
XX
XX AA94325;
AC
XX 11-AUG-2000 (first entry)
XX
XX Human seven transmembrane receptor VSHK-1.
XX
XX Human; seven transmembrane receptor; VSHK-1; signal transduction.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 6..8
XX Modified-site /note= "potential N-glycosylation site"
XX Modified-site /note= "potential N-glycosylation site"
XX Domain 42..66
XX Domain /label= Transmembrane_domain
XX Domain 79..100
XX Domain /label= Transmembrane_domain
XX Domain 114..135
XX Domain /label= Transmembrane_domain
XX Domain 156..175
XX Domain /label= Transmembrane_domain
XX Domain 199..221
XX Domain /label= Transmembrane_domain
XX Domain 241..262
XX Modified-site /label= Transmembrane_domain
XX Modified-site 276..278
XX Domain /note= "potential N-glycosylation site"
XX Domain 287..308
XX Domain /label= Transmembrane_domain

W0200026369-A1.
PD 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-US25848.
XX
XX 04-NOV-1998; 98US-0107112.
PR 06-JUN-1999; 99US-0114856.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Khoja H, Shymala V;
PI WPI: 2000-365618/31.
XX
XX N-PSDB: AA94325.
DR
XX
XX Novel polypeptide comprising a new seven-transmembrane receptor protein
XX and its encoding polynucleotide, useful for the analysis of VSHK-1.
XX
XX Claim 3: Fig 1; 79pp; English.
XX
XX The present sequence is VSHK-1, a new seven transmembrane
XX receptor which contains seven membrane-spanning helical domains
XX that are linked by three intracellular and three extracellular loops. The
XX gene sequence encoding VSHK-1 was isolated from a cDNA library in heart
XX tissue, where VSHK-1 is predominantly found, three RNA species were
XX identified: a 1.3kb; a 2.0kb; and a 5.0kb species. The polynucleotide
XX encoding the present sequence corresponds to the 2.0kb form. The 1.3kb
XX form may result from the use of an alternative polyadenylation site while
XX transcription of a 3.0kb intron at nucleotide 74 could account for the
XX 5.0kb species. VSHK-1 polynucleotides can be used as hybridisation probes

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 6, 2002, 18:04:30 ; Search time 13.09 Seconds
(Without alignments) 653.091 Million cell updates/sec

Title: US-09-686-020A-2
Perfect score: 1819
Sequence: 1 MALEONOSDIYEEENMNG.....VEEPDSEGTPEPTSF1 350

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTC05.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	US-08-966-316-16
2	1620	89.1	350	2	US-08-966-316-18
3	659	36.2	358	1	US-08-153-848-19
4	659	36.2	358	1	US-09-299-843A-19
5	659	36.2	358	4	US-09-088-337B-19
6	659	36.2	358	5	PCT-US93-11153-19
7	659	36.2	378	1	US-08-153-848-15
8	659	36.2	378	3	US-09-299-843A-15
9	659	36.2	378	4	US-09-251-545-1
10	659	36.2	378	5	US-09-088-337B-15
11	659	36.2	378	5	PCT-US93-11153-15
12	659	36.2	410	1	US-08-153-848-7
13	659	36.2	410	3	US-09-299-843A-7
14	659	36.2	410	3	US-09-088-337B-7
15	659	36.2	410	5	PCT-US93-11153-7
16	650	35.7	378	3	US-09-299-843A-66
17	650	35.7	378	4	US-09-088-337B-66
18	643	35.3	378	1	US-08-383-750-2
19	643	35.3	378	1	US-08-383-751A-2
20	643	35.3	378	3	US-08-352-678-2
21	643	35.3	378	4	US-09-045-583-49
22	643	35.3	378	5	PCT-US93-09636-2
23	637	35.0	357	4	US-09-266-464-2
24	635.5	34.9	359	1	US-08-153-848-24
25	635.5	34.9	359	1	US-09-299-843A-24
26	635.5	34.9	359	4	US-09-088-337B-24
27	635.5	34.9	359	5	PCT-US93-11153-24

28	606.5	33.3	361	2	US-08-902-294-2	Sequence 2, Appl
29	606.5	33.3	361	3	US-09-178-637-2	Sequence 2, Appl
30	583	32.1	374	4	US-09-045-583-48	Sequence 48, Appl
31	581	31.9	342	4	US-09-116-498-4	Sequence 6, Appl
32	569	31.3	342	4	US-09-116-498-6	Sequence 2, Appl
33	560	30.8	342	2	US-08-742-011-2	Sequence 2, Appl
34	560	30.8	342	4	US-09-275-384B-5	Sequence 5, Appl
35	560	30.8	342	4	US-09-116-498-2	Sequence 2, Appl
36	560	30.8	342	4	US-09-449-437A-2	Sequence 20, Appl
37	537.5	29.5	360	4	US-08-875-573-20	Sequence 20, Appl
38	537.5	29.5	360	4	US-09-232-878-2	Sequence 2, Appl
39	537.5	29.5	360	4	US-09-045-583-55	Sequence 55, Appl
40	534.5	29.4	355	1	US-07-759-568-1	Sequence 1, Appl
41	534.5	29.4	355	1	US-08-450-393A-8	Sequence 8, Appl
42	534.5	29.4	355	2	US-08-390-000A-5	Sequence 8, Appl
43	534.5	29.4	355	4	US-08-446-669-8	Sequence 8, Appl
44	534.5	29.4	355	5	PCT-US93-00476-8	Sequence 8, Appl
45	534.5	29.4	360	1	US-08-202-056-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-966-316-16
Sequence 16, Application US/08966316
Patent No. 5932445
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Roopa
APPLICANT: Murthy, Lynn F.
APPLICANT: Mathur, Preeti
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/966,316
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0424 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: UTRSNOT11
CLONE: 2547002
US-08-966-316-16

Query Match 100.0%; Score 1819; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 7.6e-148;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MALEONOSTDYEEENEMNGTIDYDSEYELICKEDEYREFAKVLPAFTIYFVIGLANS 60
 1 MALEONOSTDYEEENEMNGTIDYDSEYELICKEDEYREFAKVLPAFTIYFVIGLANS 60
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 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLKMKNIRKISRLK 240
 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLKMKNIRKISRLK 240
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 241 VLTAVIVFIVTQLPYNIIVKFCRAIDIIYSLTSCNMSKRMIDIAIOVTSIALFHSCLNP 300
 301 ILYVFMGASFKNYVAKKYGSMROROSVEEPFDESGPTSTFESI 350
 301 ILYVFMGASFKNYVAKKYGSMROROSVEEPFDESGPTSTFESI 350

RESULT 2

US-08-966-316-18
 Sequence 18, Application US/08966316
 Patent No. 5932445

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
 APPLICANT: Au-Young, Janice
 APPLICANT: Reddy, Koopa
 APPLICANT: Murry, Lynn E.
 APPLICANT: Mathur, Preete
 TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA

ZIP: 94304
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/966,316
 FILING DATE: Herewith

CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

FILING DATE:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0424 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166

TELEX:
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 350 amino acids
 TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Genbank
 CLONE: 399711
 US-08-966-316-18

Query Match 89.1%; Score 1620; DB 2; Length 350;
 Best Local Similarity 86.0%; Pred. No. 7.1e-131;
 Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

1 MALEONOSTDYEEENEMNGTIDYDSEYELICKEDEYREFAKVLPAFTIYFVIGLANS 60
 1 MALEONOSTDYEEENEMNGTIDYDSEYELICKEDEYREFAKVLPAFTIYFVIGLANS 60
 61 MVAIAVYKRTKTDYIILNLAVALDLFLFTLPFAVNAVHGVGLKIMCKITSALT 120
 61 MVAIAVYKRTKTDYIILNLAVALDLFLFTLPFAVNAVHGVGLKIMCKITSALT 120
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 241 VLTAVIVFIVTQLPYNIIVKFCRAIDIIYSLTSCNMSKRMIDIAIOVTSIALFHSCLNP 300
 241 VLTAVIVFIVTQLPYNIIVKFCRAIDIIYSLTSCNMSKRMIDIAIOVTSIALFHSCLNP 300
 301 ILYVFMGASFKNYVAKKYGSMROROSVEEPFDESGPTSTFESI 350
 301 ILYVFMGASFKNYVAKKYGSMROROSVEEPFDESGPTSTFESI 350

RESULT 3

US-08-153-848-19
 Sequence 19, Application US/08153848
 Patent No. 5759804

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald
 APPLICANT: Gray, Patrick W.
 APPLICANT: Schwellkart, Vicki L.
 TITLE OF INVENTION: No. 5759804e1 seven Transmembrane Receptors
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Bicknell
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA

ZIP: 60606
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/153,848

FILING DATE:
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/977,452

ATTORNEY/AGENT INFORMATION:
 FILING DATE: 17-NOV-1992
 NAME: No. 5759804and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31794

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300